

01PE

CRF Errors Corrected by the STIC System Branch

CRF Processing Date: 2/3/2001

Serial Number: 09/821,812

ENTERED

Edited by:                       
Verified by:                      (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:  
\_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:  
\_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  
\_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  
\_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:  
\_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:  
\_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically:  
\_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:  
\_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: globally corrected spelling of "Sapient"

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

## RAW SEQUENCE LISTING

DATE: 07/03/2001

PATENT APPLICATION: US/09/821,812

TIME: 15:07:19

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I821812.raw

PS

```

4 <110> APPLICANT: Lin, Biaoyang
6 <120> TITLE OF INVENTION: Androgen Regulated Prostate Specific
7   Nucleic Acids
9 <130> FILE REFERENCE: P-IS 4373
11 <140> CURRENT APPLICATION NUMBER: US 09/821,812
12 <141> CURRENT FILING DATE: 2001-03-28
14 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1026
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
24 tagtttgtat ttttcattac cagcaagggt aaacagttat ccatgaccca tttctatggt 60
25 ctctgtggcat gcttccatgt actgcctctg catgcagcag gccacctcgg gcagagccta 120
26 aagcatgtga taaatgaaat gctatcacaa tacagggtgt gtctgaaaaa caaatggcaa 180
27 cttattatcc aagatcaatg aaggaaaaag caaatttact aaaatatttc tttatttgaa 240
28 taaggtcaat gccatttctt gaattccagc tagcatcaaa taatcaggaa aaaaaaaact 300
29 tgacaaaatg ttatccaatt gaaattgaca gtggatagaa aaccctttta aactttaagt 360
30 aatgtcataa aagaaatata ttaaacaagc aacagacaga tctaaaaagt tccaagtgtg 420
31 gatttcacat tagatcttat aaattaaaaa aatcctcaat ataatcattt gttcactatc 480
32 ttctttcaat aagcacatgg acagggaaaag ataatcacac cttaatatcc acaactgcta 540
33 tttgtgttct ttacaaaaat tgtatctctg caatgcagtg aggcaggcaa tcccttggtc 600
34 aagtcatttc tgttttccct aagttatcaa aaagtacaac tgtctgatat aaattgttac 660
35 cataatcaca atcaggaagg caaagaagct ttagcaggca ggcttgaaga tgggagtttt 720
36 catggcttga ccatgaatga tctcaagatg atttcataag attaaaaagc atcacgaaaa 780
37 tactgaaagc aacaggtaat aatctggatt cagtctgtag ttgctcatga accacgcgtt 840
38 ttaataaaaag gaacattaag taaattgtag gtataaaaaga atcagtgcat atctgttaat 900
39 gtcattgaca ataaaaatat attatcttct cagctcagct cttaaattaac aaaacaccta 960
40 tttttttttt cccactcctc atttttagtgg ttctcaaaca ttggtgtgct cagaatctcc 1020
41 tgaggt 1026
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44 <211> LENGTH: 4527
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (96)...(851)
52 <400> SEQUENCE: 2
53 tccttggggtt cgggtgaaag cgcttggggg ttcgtggcca tgatccccga gctgctggag 60
54 aactgaaggc ggacagctct ctgcgaaacc aggca atg gcg gag ctg gag ttt 113
55                                     Met Ala Glu Leu Glu Phe
56                                     1                               5
58 gtt cag atc atc atc atc gtg gtg gtg atg atg gtg atg gtg gtg 161
59 Val Gln Ile Ile Ile Val Val Val Met Met Val Met Val Val Val
60                                     10                               20
62 atc acg tgc ctg agc cac tac aag ctg tct gca cgg tcc ttc atc 209

```

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I821812.raw

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63 Ile Thr Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile
64          25          30          35
66 agc cgg cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa 257
67 Ser Arg His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu
68          40          45          50
70 gga tgc ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca 305
71 Gly Cys Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro
72 55          60          65          70
74 gag ccg cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg 353
75 Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val
76          75          80          85
78 ccg ccc ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat 401
79 Pro Pro Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr
80          90          95          100
82 ccg tac ctg cag cac gag atc gac ctg cca ccc acc atc tcg ctg tca 449
83 Pro Tyr Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser
84          105          110          115
86 gac ggg gag gag ccc cca ccc tac cag ggc ccc tgc acc ctc cag ctt 497
87 Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu
88          120          125          130
90 cgg gac ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca 545
91 Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala
92 135          140          145          150
94 ccc cca aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg 593
95 Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg
96          155          160          165
98 ctg ggc ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg 641
99 Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Thr
100          170          175          180
102 tgc tac ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc 689
103 Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser
104          185          190          195
106 gag gtc atc ggc cac tac ccg ggg tcc tcc ttc cag cac cag cag agc 737
107 Glu Val Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln Ser
108          200          205          210
110 agt ggg ccg ccc tcc ttg ctg gag ggg acc cgg ctc cac cac aca cac 785
111 Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His
112 215          220          225          230
114 atc gcg ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa 833
115 Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys
116          235          240          245
118 cag aaa gga cac cct ctc taggggtcccc agggggggccg ggctgggggct 881
119 Gln Lys Gly His Pro Leu
120          250
122 gcgtaggtga aaaggcagaa cactccgcgc ttcttagaag aggagtgaga ggaaggcggg 941
123 gggcgagca acgcatcgtg tggccctccc ctccacctc cctgtgtata aatatttaca 1001
124 tgtgatgtct ggtctgaatg cacaagctaa gagagcttgc aaaaaaaaaa agaaaaaaga 1061
125 aaaaaaaaaa ccacgtttct ttgttgagct gtgtcttgaa ggcaaaaagaa aaaaaatttc 1121
126 tacagtagtc tttcttgttt ctagttgagc tgcgtgcgtg aatgcttatt ttcttttgtt 1181

```

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Input Set : A:\Pto.amc

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```

127 tatgataatt tcacttaact ttaaagacat atttgcacaa aacctttgtt taaagatctg 1241
128 caatattata tatataaata tatataagat aagagaaact gtatgtgcga gggcaggagt 1301
129 atttttgtat tagaagaggc ctattaaaaa aaaaagtgtt tttctgaact agaagaggaa 1361
130 aaaaatggca atttttgagt gccaaagtcag aaagtgtgta ttaccttgta aagaaaaaaa 1421
131 ttacaaagca ggggtttaga gttatttata taaatgttga gattttgcac tattttttaa 1481
132 tataaatatg tcagtgcttg cttgatggaa acctctcttg tgtctgttga gactttaagg 1541
133 gagaaatgct ggaatttcag agtcgcctga cggcagaggg tgagcccccg tggagtctgc 1601
134 agagaggcct tggccaggag cggcgggctt tcccagaggg ccactgtccc tgcagagtgg 1661
135 atgcttctgc ctagtgcag gttatcacca cgttatatat tccctaccga aggagacacc 1721
136 ttttcccccc tgaccagaa cagcctttaa atcacaaagca aaataggaaa gttaaccacg 1781
137 gaggcaccga gttccaggta gtggttttgc ctttcccaa aatgaaaata aactgttacc 1841
138 gaaggaatta gtttttcttc ttcttttttc caactgtgaa ggtccccgtg ggggtggagca 1901
139 tgggtccccc cacaagccgc agcggctggt gcccgggcta ccaggacat gccagagggc 1961
140 tcgatgactt gtctctgcag ggcgctttgg tgggtgttca gctggctaaa ggttcaccgg 2021
141 tgaaggcagg tgcggttaact gccgcactgg accctaggaa gccccaggta ttcgcaatct 2081
142 gacctcctcc tgtctgtttc ctttcacgga tcaattctca cttaagaggc caataaacia 2141
143 cccaacatga aaaggtgaca agcctgggtt tctcccagga taggtgaaag ggttaaaatg 2201
144 agtaaagcag ttgagcaaac accaaccgga gcttcgggcg cagaattctt caccttctct 2261
145 tcccctttcc atctcctttc cccgcggaaa caacgcttcc cttctggtgt gtctgttgat 2321
146 ctgtgttttc atttacatct ctcttagact ccgctcttgt tctccagggt ttcaccagat 2381
147 agatttgagg ttggcgggac ctgctggtga cgtgcagggt aaggacagga aggggcatgt 2441
148 gagcgtaaat agaggtgacc agaggagagc atgaggggtg gggctttggg acccaccggg 2501
149 gccagtggct ggagcttgac gtctttcttc cccatggggg tgggagggcc cccagctgga 2561
150 agagcagact cccagctgct accccctccc ttcccatggg agtggctttc cattttgggc 2621
151 agaatgctga ctagttagct aacataaaaag atataaaaag caataactat tgtttgtgag 2681
152 caactttttt ataacttcca aaacaaaaac ctgagcacag ttttgaagtt ctaggcactc 2741
153 gagctcctac atgtgaaacg tgtgctttac gaaggtggca gctgacagac gtgggctctg 2801
154 catgcccga gcctagtaga aagtctctgt tcattggcaa cagcagaacc tgcctctccg 2861
155 tgaagtcgtc agcctaaaat ttgtttctct cttgaagagg attctttgaa aaggtcctgc 2921
156 agagaaatca gtacaggtta tcccgaaggg tacaaggacg cacttgtaaa gatgattaaa 2981
157 acgtatcttt cctttatgtg acgcgtctct agtgccttac tgaagaagca gtgacactcc 3041
158 cgtcgtcctg tgaggacgtt cccggacagt gcctcactca cctgggactg gtatccccctc 3101
159 ccagggtcca ccaagggtct ctgcttttca gacaccccat catcctcgcg cgtcctcacc 3161
160 ctgtctctac caggaggtg cctagcttgg tgaggttact cctgctctc caaccttttt 3221
161 ttgccaaggt ttgtacacga ctcccatcta ggctgaaaac ctagaagtgg acctgtgtgtg 3281
162 tgtgcatggt gtcagcccaa agccaggctg agacagtcct catatcctct tgagccaaac 3341
163 tgtttgggtc tcgttgcttc atggtatggt ctggatttgt gggaatggct ttgcgtgaga 3401
164 aaggggagga gagtgtgtgc tgccctcagc cggcttgagg acagagcctg tccctctcat 3461
165 gacaactcag tgttgaagcc cagtgtcctc agcttcatgt ccagtggatg gcagaagttc 3521
166 atggggtagt ggctctcaa aggetgggag catcccaaga cagccagcag gttgtctctg 3581
167 gaaacgacca gagttaagct ctcggtctct ctgctgaggg tgcacccttt cctctagatg 3641
168 gtagttgtca cgttatcttt gaaaactctt ggactgctcc tgaggaggcc ctcttttcca 3701
169 gtaggaagtt agatgggggt tctcagaagt ggctgattgg aaggggacaa gcttcgtttc 3761
170 aggggtctgc cgttccatcc tgggtcagag aaggccgagc gtggctttct ctagccttgt 3821
171 cactgtctcc ctgctgtca atcaccacct ttccyccaga ggaggaaaat tatctccctc 3881
172 gcaaagcccg gttctacaca gatttcacaa attgtgctaa gaaccgtccg tgttctcaga 3941
173 aagcccagtg tttttgcaaa gaatgaaaag ggacccata thtagcaaaa atcagggtctg 4001
174 ggggagagcc gggttcattc cctgtcctca ttggtcgtcc ctatgaattg tacgtttcag 4061
175 agaaattttt tttcctatgt gcaacacgaa gcttccagaa ccataaaaata tcccgtcgat 4121

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## RAW SEQUENCE LISTING

DATE: 07/03/2001

PATENT APPLICATION: US/09/821,812

TIME: 15:07:19

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I821812.raw

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176 aaggaaagaa aatgtcgttg ttgttgtttt tctggaaact gcttgaaatc ttgctgtact 4181
177 atagagctca gaaggacaca gcccgtcctc ccctgcctgc ctgattccat ggctgttggtg 4241
178 ctgattccaa tgctttcacg ttggttcctg gcgtgggaac tgctctcctt tgcagcccca 4301
179 tttcccaagc tctgttcaag ttaaacttat gtaagctttc cgtggcatgc ggggcgcgca 4361
180 cccacgtccc cgctgcgtaa gactctgtat ttggatgcca atccacaggc ctgaagaaac 4421
181 tgcttggtgt gtatcagtaa tcattagtgg caatgatgac attctgaaaa gctgcaatac 4481
182 ttatacaata aattitacaa ttctttggaa aaaaaaaaaa aaaaaa 4527

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184 &lt;210&gt; SEQ ID NO: 3

185 &lt;211&gt; LENGTH: 252

186 &lt;212&gt; TYPE: PRT

187 &lt;213&gt; ORGANISM: Homo sapiens

189 &lt;400&gt; SEQUENCE: 3

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190 Met Ala Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val Val Met
191 1 5 10 15
192 Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His Tyr Lys Leu
193 20 25 30
194 Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg Glu
195 35 40 45
196 Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr Val
197 50 55 60
198 Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro
199 65 70 75 80
200 Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe His
201 85 90 95
202 Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu Pro
203 100 105 110
204 Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly
205 115 120 125
206 Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn
207 130 135 140
208 Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp
209 145 150 155 160
210 Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn
211 165 170 175
212 Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly
213 180 185 190
214 Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser
215 195 200 205
216 Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr
217 210 215 220
218 Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp
219 225 230 235 240
220 Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
221 245 250

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224 &lt;210&gt; SEQ ID NO: 4

225 &lt;211&gt; LENGTH: 2213

226 &lt;212&gt; TYPE: DNA

227 &lt;213&gt; ORGANISM: Homo sapiens

229 &lt;220&gt; FEATURE:

## RAW SEQUENCE LISTING

DATE: 07/03/2001

PATENT APPLICATION: US/09/821,812

TIME: 15:07:19

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I821812.raw

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230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)...(1611)
233 <221> NAME/KEY: misc_feature
234 <222> LOCATION: (1)...(2213)
235 <223> OTHER INFORMATION: Xaa=any amino acid
237 <400> SEQUENCE: 4
238 ggg ggg ctg aca aca act gtg ata ggt acg agg ctg ggt gtg gat cgg 48
239 Gly Gly Leu Thr Thr Val Ile Gly Thr Arg Leu Gly Val Asp Arg
240 1 5 10 15
242 ccg agg ctc tcc tgg agc gct ggg cct tcg ctg gcc gca ccg gca gcc 96
243 Pro Arg Leu Ser Trp Ser Ala Gly Pro Ser Leu Ala Ala Pro Ala Ala
244 20 25 30
246 atg agc tcg gag atg gag ccg ctg ctc ctg gcc tgg agc tat ttt agg 144
247 Met Ser Ser Glu Met Glu Pro Leu Leu Leu Ala Trp Ser Tyr Phe Arg
248 35 40 45
250 cgc agg aag ttc cag ctc tgc gcc gat cta tgc acg cag atg ctg gag 192
251 Arg Arg Lys Phe Gln Leu Cys Ala Asp Leu Cys Thr Gln Met Leu Glu
252 50 55 60
254 aag tcc cct tat gac cag gca gct tgg atc tta aaa gca aga gcg cta 240
255 Lys Ser Pro Tyr Asp Gln Ala Ala Trp Ile Leu Lys Ala Arg Ala Leu
256 65 70 75 80
258 aca gaa atg gta tac ata gat gaa att gat gta gat cag gaa gga att 288
259 Thr Glu Met Val Tyr Ile Asp Glu Ile Asp Val Asp Gln Glu Gly Ile
260 85 90 95
262 gca gaa atg atg ctg gat gaa aat gct ata gct caa gtt cca cgc cct 336
263 Ala Glu Met Met Leu Asp Glu Asn Ala Ile Ala Gln Val Pro Arg Pro
264 100 105 110
266 gga acg tct ttg aaa ctc cct gga act aat cag aca gga ggg cct agc 384
267 Gly Thr Ser Leu Lys Leu Pro Gly Thr Asn Gln Thr Gly Gly Pro Ser
268 115 120 125
270 cag gcc gtt agg cca atc aca caa gct gga aga ccc att aca ggt ttc 432
271 Gln Ala Val Arg Pro Ile Thr Gln Ala Gly Arg Pro Ile Thr Gly Phe
272 130 135 140
274 ctc agg ccc agc acg cag agt gga agg cca ggc act atg gaa cag gct 480
275 Leu Arg Pro Ser Thr Gln Ser Gly Arg Pro Gly Thr Met Glu Gln Ala
276 145 150 155 160
278 atc aga aca ccc aga acc gcc tac aca gcc cgc cct atc acc agc tcc 528
279 Ile Arg Thr Pro Arg Thr Ala Tyr Thr Ala Arg Pro Ile Thr Ser Ser
280 165 170 175
282 tcc gga aga ttt gtc agg ctg gga acg gct tcc atg ctt aca agt cct 576
283 Ser Gly Arg Phe Val Arg Leu Gly Thr Ala Ser Met Leu Thr Ser Pro
284 180 185 190
286 gat gga cca ttt ata aat tta tct agg ctg aat tta aca aag tat tcc 624
287 Asp Gly Pro Phe Ile Asn Leu Ser Arg Leu Asn Leu Thr Lys Tyr Ser
288 195 200 205
290 cag aaa cct aag ttg gca aag gct tgt ttg agt ata tct ttc atc atg 672
291 Gln Lys Pro Lys Leu Ala Lys Ala Cys Leu Ser Ile Ser Phe Ile Met
292 210 215 220
294 aaa atg atg tta aga ctg ctt tgg atc tgg ctg gcc ctc tcc aca gaa 720

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/821,812

DATE: 07/03/2001

TIME: 15:07:20

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I821812.raw

L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/821,812

DATE: 06/15/2001

TIME: 17:16:38

Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

P-5

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Lin, Biaoyang  
 6 <120> TITLE OF INVENTION: Androgen Regulated Prostate Specific  
 7 Nucleic Acids  
 9 <130> FILE REFERENCE: P-IS 4373  
 11 <140> CURRENT APPLICATION NUMBER: US 09/821,812  
 12 <141> CURRENT FILING DATE: 2001-03-28  
 14 <160> NUMBER OF SEQ ID NOS: 11  
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1026  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Homo sapiens  
 23 <400> SEQUENCE: 1  
 24 tagtttgtat ttttcattac cagcaagggg aaacagttat ccatgaccca tttctatgtt 60  
 25 ctctgtggcat gcttccatgt actgcctctg catgcagcag gccacctcgg gcagagccta 120  
 26 aagcatgtga taaatgaaat gctatcacia tacaggttgt gtctgaaaaa caaatggcaa 180  
 27 cttattatcc aagatcaatg aaggaaaaag caaatctact aaaatatttc tttatttgaa 240  
 28 taaggtcaat gccatttctt gaattccagc tagcatcaaa taatcaggaa aaaaaaaact 300  
 29 tgacaaaaatg ttatccaatt gaaattgaca gtggatagaa aaccttttta aactttaagt 360  
 30 aatgtcataa aagaaatata ttaacaagc aacagacaga tctaaaaagt tccaagtgtg 420  
 31 gatttcacat tagatcttat aaattaaaaa aatcctcaat ataatcattt gttcactatc 480  
 32 ttctttcaat aagcacatgg acagggaag ataatcacac cttaatatcc acaactgcta 540  
 33 tttgtgttct ttacaaaaat tgtatctctg caatgcagtg aggcaggcaa tcccttggtc 600  
 34 aagtcatttc tgttttcctt aagttatcaa aaagtacaac tgtctgatat aaattgttac 660  
 35 cataatcaca atcaggaagg caaagaagct ttagcaggca ggcttgaaga tgggagtttt 720  
 36 catggcttga ccatgaatga tctcaagatg atttcataag attaaaagcc atcacgaaaa 780  
 37 tactgaaagc aacaggtaat aatctggatt cagctctgtg ttgctcatga accacgcgtt 840  
 38 ttaataaaag gaacattaag taaattgtag gtataaaaga atcagtgcat atctgttaat 900  
 39 gtcattgaca ataaaaatat attatcttct cagctcagct ctaaaattaac aaaacaccta 960  
 40 tttttttttt cccactcctc attttagtgg ttctcaaaca ttggtgtgct cagaatctcc 1020  
 41 tgaggt 1026  
 43 <210> SEQ ID NO: 2  
 44 <211> LENGTH: 4527  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Homo sapiens  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: CDS  
 50 <222> LOCATION: (96)...(851)  
 52 <400> SEQUENCE: 2  
 53 tccttgggtt cgggtgaaag cgcttggggg ttctgtggcca tgatccccga gctgctggag 60  
 54 aactgaaggc ggacagtctc ctgcgaaacc aggca atg gcg gag ctg gag ttt 113  
 55 Met Ala Glu Leu Glu Phe  
 56 1 5  
 58 gtt cag atc atc atc atc gtg gtg gtg atg atg gtg atg gtg gtg gtg 161  
 59 Val Gln Ile Ile Ile Ile Val Val Val Met Met Val Met Val Val Val  
 60 10 15 20  
 62 atc acg tgc ctg ctg agc cac tac aag ctg tct gca cgg tcc ttc atc 209



## RAW SEQUENCE LISTING

DATE: 06/15/2001

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TIME: 17:16:38

Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

```

63 Ile Thr Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile
64      25      30      35
66 agc cgg cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa 257
67 Ser Arg His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu
68      40      45      50
70 gga tgc ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca 305
71 Gly Cys Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro
72 55      60      65      70
74 gag ccg cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg 353
75 Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val
76      75      80      85
78 ccg ccc ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat 401
79 Pro Pro Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr
80      90      95      100
82 ccg tac ctg cag cac gag atc gac ctg cca ccc acc atc tcg ctg tca 449
83 Pro Tyr Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser
84      105      110      115
86 gac ggg gag gag ccc cca ccc tac cag ggc ccc tgc acc ctc cag ctt 497
87 Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu
88      120      125      130
90 cgg gac ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca 545
91 Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala
92 135      140      145      150
94 ccc cca aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg 593
95 Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg
96      155      160      165
98 ctg ggc ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg 641
99 Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Thr
100      170      175      180
102 tgc tac ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc 689
103 Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser
104      185      190      195
106 gag gtc atc ggc cac tac ccg ggg tcc tcc ttc cag cac cag cag agc 737
107 Glu Val Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln Ser
108      200      205      210
110 agt ggg ccg ccc tcc ttg ctg gag ggg acc cgg ctc cac cac aca cac 785
111 Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His
112 215      220      225      230
114 atc gcg ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa 833
115 Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys
116      235      240      245
118 cag aaa gga cac cct ctc taggggtcccc agggggggccg ggctggggct 881
119 Gln Lys Gly His Pro Leu
120      250
122 gcgtaggtga aaaggcagaa cactccgcgc ttcttagaag aggagtgaga ggaaggcggg 941
123 gggcgagca acgcacgtg tggccctccc ctcccacctc cctgtgtata aatatttaca 1001
124 tgtgatgtct ggtctgaatg cacaagctaa gagagcttgc aaaaaaaaaa agaaaaaaga 1061
125 aaaaaaaaaa ccacgtttct ttgttgagct gtgtcttgaa ggcaaaagaa aaaaaatttc 1121
126 tacagtagtc tttcttgttt ctagttgagc tgcgtgcgtg aatgcttatt ttcttttgtt 1181

```

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TIME: 17:16:38

Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

```

127 tatgataatt tcacttaact ttaaagacat atttgcacaa aacctttgtt taaagatctg 1241
128 caatattata tatataaata tatataagat aagagaaact gtatgtgcga gggcaggagt 1301
129 atttttgtat tagaagaggc ctattaaaaa aaaaagttgt tttctgaact agaagaggaa 1361
130 aaaaatggca atttttgagt gccaaagtcag aaagtgtgta ttaccttgta aagaaaaaaa 1421
131 ttacaaagca ggggtttaga gttatttata taaatgttga gattttgcac tattttttta 1481
132 tataaatatg tcagtgtctg cttgatggaa acctctcttg tgtctgttga gactttaagg 1541
133 gagaaatgtc ggaatttcag agtcgcctga cggcagaggg tgagcccccg tggagtctgc 1601
134 agagaggcct tggccaggag cggcgggctt tcccgagggg ccactgtccc tgcagagtgg 1661
135 atgcttctgc ctagtgacag gttatcacca cgttatatat tccctaccga aggagacacc 1721
136 ttttccccc tgacccagaa cagcctttaa atcacaagca aaataggaaa gttaaccacg 1781
137 gaggcaccga gttccaggta gtggttttgc ctttcccaaa aatgaaaata aactgttacc 1841
138 gaaggaatta gtttttctc ttcttttttc caactgtgaa ggtccccgtg ggggtggagca 1901
139 tgggtcccc cacaagccgc agcggctggg gcccgggcta ccagggacat gccagagggc 1961
140 tcgatgactt gtctctgcag ggcgctttgg tggttgttca gctggctaaa ggttcaccgg 2021
141 tgaaggcagg tgcggtaact gcgcactgg acctaggaa gcccaggta ttcgcaatct 2081
142 gacctctctc tgtctgtttc ccttcacgga tcaattctca cttaaagggc caataaaca 2141
143 cccaacatga aaagggtgaca agcctggggt tctccaggga taggtgaaag ggttaaaatg 2201
144 agtaaagcag ttgagcaaac accaaccgga gcttcgggcg cagaattctt caccttctct 2261
145 tcccccttcc atctcctttc ccgcgggaaa caacgcttcc cttctggtgt gtctgttgat 2321
146 ctgtgttttc atttacctct ctcttagact ccgctcttgt tctccagggt ttcaccagat 2381
147 agatttgagg ttggcgggac ctgctggtga cgtgcagggt aaggacagga aggggcatgt 2441
148 gagcgtaaag agaggtgacc agaggagagc atgaggggtg gggctttggg acccaccggg 2501
149 gccagtggct ggagcttgac gtctttctc cccatggggg tgggagggcc cccagctgga 2561
150 agagcagact cccagctgct accccctccc tcccatggg agtggcttcc cattttgggc 2621
151 agaatgctga ctagtagact aacataaaaag atataaaaag caataactat tgtttgtgag 2681
152 caactttttt ataacttcca aaacaaaaac ctgagcacag ttttgaagtt ctagccactc 2741
153 gagctcatgc atgtgaaacg tgtgctttac gaagggtggca gctgacagac gtgggctctg 2801
154 catgccgcca gcttagtaga aagttctcgt tcattggcaa cagcagaacc tgectctccg 2861
155 tgaagtcgtc agcctaaaaat ttgtttctct cttgaagagg attctttgaa aaggctctgc 2921
156 agagaaatca gtacagggtta tcccgaagg tacaaggacg cacttgtaaa gatgattaaa 2981
157 acgtatcttt cctttatgtg acgctctctc agtgccctac tgaagaagca gtgacactcc 3041
158 cgtcgtctgg tgaggacgtt ccgggacagt gcctcactca cctgggactg gtatccctcc 3101
159 ccagggtcca ccaagggtc cctgttttca gacaccccat catcctcgcg cgtcctcacc 3161
160 ctgtctctac cagggaggtg cctagcttgg tgaggttact cctgctcctc caaccttttt 3221
161 ttgccaaggt ttgtacacga ctcccatcta ggctgaaaac ctagaagtgg accttgtgtg 3281
162 tgtgcatggg gtcagcccaa agccaggctg agacagtcct catatctctt tgagccaaac 3341
163 tgtttgggtc tcgttgcttc atggtatggg ctggatttgt gggaaatggc ttgctgaga 3401
164 aaggggagga gagtggttgc tgcctcagc cggcttgagg acagagcctg tccctctcat 3461
165 gacaactcag tgttgaagcc cagtgtctc agcttcatgt ccagtggatg gcagaagttc 3521
166 atggggtagt ggcctctcaa aggctgggcg catcccaaga cagccagcag gttgtctctg 3581
167 gaaacgacca gagttaagct ctcggtctct ctgctgaggg tgcaccttt cctctagatg 3641
168 gtagttgtca cgttatcttt gaaaactctt ggactgctcc tgaggaggcc ctcttttcca 3701
169 gtaggaagtt agatgggggt tctcagaagt ggctgattgg aaggggacaa gcttcgtttc 3761
170 aggggtctgc cgttccatcc tggttcagag aaggccgagc gtggctttct ctagecctgt 3821
171 cactgtctcc ctgctgtca atcaccacct ttccyccaga ggaggaaaat tatctccct 3881
172 gcaaagcccg gttctacaca gatttcacaa attgtgctaa gaaccgtccg tgttctcaga 3941
173 aagcccagtg tttttgcaaa gaatgaaaag ggaccccata tgtagcaaaa atcagggtctg 4001
174 ggggagagcc gggttcattc cctgtctcct ttggtcgtcc ctatgaattg tacgtttcag 4061
175 agaaattttt tttcctatgt gcaacacgaa gcttcacgaa ccataaaata tcccgctcat 4121

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## RAW SEQUENCE LISTING

DATE: 06/15/2001

PATENT APPLICATION: US/09/821,812

TIME: 17:16:38

Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

```

176 aaggaaagaa aatgtcgttg ttgttgtttt tctggaaact gcttgaaatc ttgctgtact 4181
177 atagagctca gaaggacaca gcccgctctc ccctgcctgc ctgattccat ggctgttggtg 4241
178 ctgattccaa tgctttcacg ttggttcctg gcgtgggaac tgctctcctt tgcagcccca 4301
179 tttcccaagc tctgttcaag ttaaacttat gtaagctttc cgtggcatgc ggggcgcgca 4361
180 cccacgtccc cgctgcgtaa gactctgtat ttggatgcca atccacaggc ctgaagaaac 4421
181 tgcttggtgt gtatcagtaa tcattagtgg caatgatgac attctgaaaa gctgcaatac 4481
182 ttatacaata aattttacaa ttctttggaa aaaaaaaaaa aaaaaa 4527

```

184 &lt;210&gt; SEQ ID NO: 3

185 &lt;211&gt; LENGTH: 252

186 &lt;212&gt; TYPE: PRT

187 &lt;213&gt; ORGANISM: Homo sapiens

189 &lt;400&gt; SEQUENCE: 3

```

190 Met Ala Glu Leu Glu Phe Val Gln Ile Ile Ile Val Val Val Met
191 1 5 10 15
192 Met Val Met Val Val Ile Thr Cys Leu Leu Ser His Tyr Lys Leu
193 20 25 30
194 Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg Glu
195 35 40 45
196 Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr Val
197 50 55 60
198 Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro
199 65 70 75 80
200 Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe His
201 85 90 95
202 Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu Pro
203 100 105 110
204 Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly
205 115 120 125
206 Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn
207 130 135 140
208 Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp
209 145 150 155 160
210 Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn
211 165 170 175
212 Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly
213 180 185 190
214 Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser
215 195 200 205
216 Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr
217 210 215 220
218 Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp
219 225 230 235 240
220 Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
221 245 250

```

224 &lt;210&gt; SEQ ID NO: 4

225 &lt;211&gt; LENGTH: 2213

226 &lt;212&gt; TYPE: DNA

227 &lt;213&gt; ORGANISM: Homo sapiens

229 &lt;220&gt; FEATURE:

## RAW SEQUENCE LISTING

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Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

```

230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)...(1611)
233 <221> NAME/KEY: misc_feature
234 <222> LOCATION: (1)...(2213)
235 <223> OTHER INFORMATION: Xaa=any amino acid
237 <400> SEQUENCE: 4
238 ggg ggg ctg aca aca act gtg ata ggt acg agg ctg ggt gtg gat cgg      48
239 Gly Gly Leu Thr Thr Thr Val Ile Gly Thr Arg Leu Gly Val Asp Arg
240 1      5      10      15
242 ccg agg ctc tcc tgg agc gct ggg cct tcg ctg gcc gca ccg gca gcc      96
243 Pro Arg Leu Ser Trp Ser Ala Gly Pro Ser Leu Ala Ala Pro Ala Ala
244      20      25      30
246 atg agc tcg gag atg gag ccg ctg ctc ctg gcc tgg agc tat ttt agg      144
247 Met Ser Ser Glu Met Glu Pro Leu Leu Leu Ala Trp Ser Tyr Phe Arg
248      35      40      45
250 cgc agg aag ttc cag ctc tgc gcc gat cta tgc acg cag atg ctg gag      192
251 Arg Arg Lys Phe Gln Leu Cys Ala Asp Leu Cys Thr Gln Met Leu Glu
252      50      55      60
254 aag tcc cct tat gac cag gca gct tgg atc tta aaa gca aga gcg cta      240
255 Lys Ser Pro Tyr Asp Gln Ala Ala Trp Ile Leu Lys Ala Arg Ala Leu
256      65      70      75      80
258 aca gaa atg gta tac ata gat gaa att gat gta gat cag gaa gga att      288
259 Thr Glu Met Val Tyr Ile Asp Glu Ile Asp Val Asp Gln Glu Gly Ile
260      85      90      95
262 gca gaa atg atg ctg gat gaa aat gct ata gct caa gtt cca cgc cct      336
263 Ala Glu Met Met Leu Asp Glu Asn Ala Ile Ala Gln Val Pro Arg Pro
264      100      105      110
266 gga acg tct ttg aaa ctc cct gga act aat cag aca gga ggg cct agc      384
267 Gly Thr Ser Leu Lys Leu Pro Gly Thr Asn Gln Thr Gly Gly Pro Ser
268      115      120      125
270 cag gcc gtt agg cca atc aca caa gct gga aga ccc att aca ggt ttc      432
271 Gln Ala Val Arg Pro Ile Thr Gln Ala Gly Arg Pro Ile Thr Gly Phe
272      130      135      140
274 ctc agg ccc agc acg cag agt gga agg cca ggc act atg gaa cag gct      480
275 Leu Arg Pro Ser Thr Gln Ser Gly Arg Pro Gly Thr Met Glu Gln Ala
276      145      150      155      160
278 atc aga aca ccc aga acc gcc tac aca gcc cgc cct atc acc agc tcc      528
279 Ile Arg Thr Pro Arg Thr Ala Tyr Thr Ala Arg Pro Ile Thr Ser Ser
280      165      170      175
282 tcc gga aga ttt gtc agg ctg gga acg gct tcc atg ctt aca agt cct      576
283 Ser Gly Arg Phe Val Arg Leu Gly Thr Ala Ser Met Leu Thr Ser Pro
284      180      185      190
286 gat gga cca ttt ata aat tta tct agg ctg aat tta aca aag tat tcc      624
287 Asp Gly Pro Phe Ile Asn Leu Ser Arg Leu Asn Leu Thr Lys Tyr Ser
288      195      200      205
290 cag aaa cct aag ttg gca aag gct tgt ttg agt ata tct ttc atc atg      672
291 Gln Lys Pro Lys Leu Ala Lys Ala Cys Leu Ser Ile Ser Phe Ile Met
292      210      215      220
294 aaa atg atg tta aga ctg ctt tgg atc tgg ctg gcc ctc tcc aca gaa      720

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 06/15/2001

PATENT APPLICATION: US/09/821,812

TIME: 17:16:39

Input Set : A:\Is4373.txt

Output Set: N:\CRF3\06152001\I821812.raw

L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9